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FIG. 1A

1	ATGCCGGCCTGCTGCAGCTGCAGTGATGTTTTCCAGTATGAGACGAACAAAGTCACTCGG	60
1	M P A C C S C S D V F Q Y E T N K V T R	20
61	ATCCAGAGCATGAATTATGGCACCATTAAAGTGGTTCTTCCACGTGATCATCTTTTCCTAC	120
21	I Q S M N Y G T <u>I K W F F H V I I F S Y</u>	40
121	GTTTGCTTTGCTCTGGTGAGTGACAAGCTGTACCAGCGGAAAGAGCCTGTCATCAGTTCT	180
41	<u>V C F A L V</u> S D K L Y Q R K E P V I S S	60
181	GTGCACACCAAGGTGAAGGGGATAGCAGAGGTGAAAGAGGAGATCGTGGAGAATGGAGTG	240
61	V H T K V K G I A E V K E E I V E N G V	80
241	AAGAAGTTGGTGACAGTGTCTTTGACACCGCAGACTACACCTTCCCTTTCAGGGGAAC	300
81	K K L V H S V F D T A D Y T F P L Q G N	100
301	TCTTTCTTCGTGATGACAACTTTCTCAAACAGAAGGCCAAGAGCAGCGGTTGTGTCCC	360
101	S F F V M T N F L K T E G Q E Q R L C P	120
361	GAGTATCCCAACCGCAGGACGCTCTGTTCTCTGACCGAGGTTGTAAAAAGGGATGGATG	420
121	E Y P T R R T L C S S D R G C K K G W M	140
421	GACCCGCAGAGCAAAGGAATTCAGACCGGAAGGTGTGTAGTGTATGAAGGGAACAGAAG	480
141	D P Q S K G I Q T G R C V V Y E G N Q K	160
481	ACCTGTGAAGTCTCTGCCTGGTGCCCCATCGAGGCAGTGGAAGAGGCCCCCGGCTGCT	540
161	T C E V S A W C P I E A V E E A P R P A	180
541	CTCTGAACAGTGCCGAAACTTCACTGTGCTCATCAAGAACAAATATCGACTTCCCCGGC	600
181	L L N S A E N F T V L I K N N I D F P G	200
601	CACAACTACACCACATACGCCAAGTACTACAAGGAAAACAATGTTGAGAAACGGACTCTG	660
201	H N Y T T Y A K Y Y K E N N V E K R T L	220
661	ATAAAAGTCTTCGGGATCCGTTTTGACATCCTGGTTTTTGGCACCGGAGGAAAATTTGAC	720
221	I K V F G I R F D I L V F G T G G K F D	240
721	ATTATCCAGCTGGTTGTGTACATCGGCTCAACCCTCTCCTACTTCGGTCTGGCCACTGTG	780
241	I I Q L <u>V V Y I G S T L S Y F G L A T V</u>	260
781	TTCATCGACTTCCTCATCGAACTTACTCCAGTAACTGCTGTCGCTCCCATATTTATCCC	840
261	<u>F I</u> D F L I D T Y S S N C C R S H I Y P	280
841	TGGTGCAAGTGCTGTGAGCCCTGTGTGGTCAACGAATACTACTACAGGAAGAAGTGCGAG	900
281	W C K C C Q P C V V N E Y Y Y R K K C E	300

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FIG. 1B

901	TCCATTGTGGAGCCAAAGCCGACATTAAAGTATGTGTCCTTTGTGGATGAATCCCACATT	960
301	S I V E P K P T L K Y V S F V D E S H I	320
961	AGGATGGTGAACCAGCAGCTACTAGGGAGAAGTCTGCAAGATGTCAAGGGCCAAGAAGTC	1020
321	R M V N Q Q L L G R S L Q D V K G Q E V	340
1021	CCAAGACCTGCGATGGACTTCACAGATTTGTCCAGGCTGCCCCTGGCCCTCCATGACACA	1080
341	P R P A M D F T D L S R L P L A L H D T	360
1081	CCCCGATTCTCTGGACAACCAGAGGAGATACGGCTGCTTAGAAAGGAGGCGACTCCTAGA	1140
361	P P I P G Q P E E I R L L R K E A T P R	380
1141	TCCAGGGATAGCCCCGTCTGGTGCCAGTGTGGAAGCTGCCTCCCATCTCAACTCCCTGAG	1200
381	S R D S P V W C Q C G S C L P S Q L P E	400
1201	AGCCACAGGTGCCTGGAGGAGCTGTGCTGCCGAAAAAGCCGGGGGCTGCATCACCACC	1260
401	S H R C L E E L C C R K K P G A C I T T	420
1261	TCAGAGCTGTTTCAGGAAGCTGGTCCTGTCCAGACACGTCCTGCAGTTCCTCCTGCTCTAC	1320
421	S E L F R K L V L S R H V L Q F L L L Y	440
1321	CAGGAGCCCTTGCTGGCGCTGGATGTGGATTCCACCAACAGCCGGCTGCGGCACTGTGCC	1380
441	Q E P L L A L D V D S T N S R L R H C A	460
1381	TACAGGTGCTACGCCACCCGGCGCTTCGGCTCCCAGGACATGGCTGACTTTGCCATCCTG	1440
461	Y R C Y A T R R F G S Q D M A D F A I L	480
1441	CCCAGCTGCTGCCGCTGGAGGATCCGGAAGAGTTTCCAAAGAGTGAAGGGCAGTACAGT	1500
481	P S C C R W R I R K E F P K S E G Q Y S	500
1501	GGCTTCAAGAGTCCTTACTGA	1521
501	G F K S P Y	506

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FIG. 2A

```

P2X7_HUMAN      ~~~~~~MPACCSCSDFQYETNKVTRIQSMNYCTIKWFFHVIIFS.YC
P2X7_VAR_HUMAN  ~~~~~~MPACCSCSDFQYETNKVTRIQSMNYCTIKWFFHVIIFS.YC
P2X7_MOUSE      ~~~~~~MPACCSWNDVFQYETNKVTRIQSTNYGTVKWLHMIIVFSY.IIS
P2X7_RAT        ~~~~~~MPACCSWNDVFQYETNKVTRIQSVNYGTVKWLHMTMFSY.VS
P2X2_HUMAN      MAAAQPKYPAGATARRLARGCWS..ALWDYETPKVIVVRNRRLGVLYRAVOLLILLYFVW
P2X3_HUMAN      ~~~~~~MNCIS..DEFTYETTKSVVVKSWTIGLINRVOLLIIISYFVG
P2X1_HUMAN      ~~~~~~MARRFQEELAA..FLFEYDTPRMVLVRNKKVGVIFRLTOLVVLVYVIG
P2X4_HUMAN      ~~~~~~MA.GCCSALAA..FLFEYDTPRTVLIRSRKVGIMNRAVOLLILAYVIG
P2X5_HUMAN      ~~~~~~MGQAGCKGLCL..SLFDYKTEKYVIAKNKKVGLLYRLLQASILAYLVV
P2X6_HUMAN      ~~~~~~MGSPGAT.TGW..GLLDYKTEKYVMTENNRVGCALORLLOFGIVVYVVG

P2X7_HUMAN      FALVSDKLYORKEP.VISSVHTKVKGIAEVKEETIVENGVKKLVSVDTDADYTFPLQG.N
P2X7_VAR_HUMAN  FALVSDKLYORKEP.VISSVHTKVKGIAEVKEETIVENGVKKLVSVDTDADYTFPLQG.N
P2X7_MOUSE      FALVSDKLYORKEP.VISSVHTKVKGIAEVTENVTEGGMTKLGHSTEDTADYTFPLQG.N
P2X7_RAT        FALVSDKLYORKEP.VISSVHTKVKGIAEVTENVTEGGMTKLGHSTEDTADYTFPLQG.N
P2X2_HUMAN      YVFTVOKSYQESSETGPESSIIITKVKGIT.....TSE.....HKVWDVVEEYVKPPEGGS
P2X3_HUMAN      WVFLHEKAYQVRDTESSVHTKVKGSG.....LYA.....NVMDVSDYVTPPQGTG
P2X1_HUMAN      WVFLYEKGYQTSS.GLISSVSVKLKGLEA.....VTQ..LPGLGPQVWDVADYVFPAQGDN
P2X4_HUMAN      WVFWWEKGYQETD.SVSSVHTKVKGVA.....VTN..TSKLGFRWDVADYVIPAQEEN
P2X5_HUMAN      WVFLIKKGYQDVTSLQSAVITKVKGVA.....FTN..TSDLGORWDVADYVIPAQGEN
P2X6_HUMAN      WALLAKKGYQERDLEPQFSIIITKLVGS.....VTQ..IKELGNRLWDVADYVFPQGEN

P2X7_HUMAN      SFFVMTNFKTEGQEQRLCPE...YPTRRTLCSDDRGCKKGWMDPQSKGIOTGRCVHVEG
P2X7_VAR_HUMAN  SFFVMTNFKTEGQEQRLCPE...YPTRRTLCSDDRGCKKGWMDPQSKGIOTGRCVHVEG
P2X7_MOUSE      SFFVMTNFKTEGQEQRLCPE...YPTRRTLCSDDRGCKKGWMDPQSKGIOTGRCVHVEG
P2X7_RAT        SFFVMTNFKTEGQEQRLCPE...YPTRRTLCSDDRGCKKGWMDPQSKGIOTGRCVHVEG
P2X2_HUMAN      VESITTRVEATHSOTOGTCPEISIRVHNAT..CLSDADCVAGELDMLGNGLRTGRCVPHYQ
P2X3_HUMAN      VFVLTITKMITVTENOMQGFCEPESEEK...CVSDSQ..GPEPLPGGGILTGRV.NYS
P2X1_HUMAN      SFFVMTNFKTEGQEQRLCPE...YPTRRTLCSDDRGCKKGWMDPQSKGIOTGRCVHVEG
P2X4_HUMAN      SFFVMTNFKTEGQEQRLCPE...YPTRRTLCSDDRGCKKGWMDPQSKGIOTGRCVHVEG
P2X5_HUMAN      SFFVMTNFKTEGQEQRLCPE...YPTRRTLCSDDRGCKKGWMDPQSKGIOTGRCVHVEG
P2X6_HUMAN      SFFVMTNFKTEGQEQRLCPE...YPTRRTLCSDDRGCKKGWMDPQSKGIOTGRCVHVEG

P2X7_HUMAN      N.QKTCEVSAWCPTEAVEEAPRPALLNSAENFTVLIKNNIDFPGHNYTTRNILPGMNI..
P2X7_VAR_HUMAN  N.QKTCEVSAWCPTEAVEEAPRPALLNSAENFTVLIKNNIDFPGHNYTTRNILPGMNI..
P2X7_MOUSE      H.RKTCEVSAWCPTEAVEEAPRPALLNSAENFTVLIKNNIDFPGHNYTTRNILPGMNI..
P2X7_RAT        K.RKTCEVSAWCPTEAVEEAPRPALLNSAENFTVLIKNNIDFPGHNYTTRNILPGMNI..
P2X2_HUMAN      GPSKTCEVSAWCPTEAVEEAPRPALLNSAENFTVLIKNNIDFPGHNYTTRNILPGMNI..
P2X3_HUMAN      SVLRTCEVSAWCPTEAVEEAPRPALLNSAENFTVLIKNNIDFPGHNYTTRNILPGMNI..
P2X1_HUMAN      HVK.TCEVSAWCPTEAVEEAPRPALLNSAENFTVLIKNNIDFPGHNYTTRNILPGMNI..
P2X4_HUMAN      SVK.TCEVSAWCPTEAVEEAPRPALLNSAENFTVLIKNNIDFPGHNYTTRNILPGMNI..
P2X5_HUMAN      LARGTCEVSAWCPTEAVEEAPRPALLNSAENFTVLIKNNIDFPGHNYTTRNILPGMNI..
P2X6_HUMAN      THR.TCEVSAWCPTEAVEEAPRPALLNSAENFTVLIKNNIDFPGHNYTTRNILPGMNI..

P2X7_HUMAN      ..TCTFHKTQNPQCFIFRLGDIFFRETGDNFSDVAIQGGIMGIEIYWDCNLDWRFHHCRPR
P2X7_VAR_HUMAN  ..TCTFHKTQNPQCFIFRLGDIFFRETGDNFSDVAIQGGIMGIEIYWDCNLDWRFHHCRPR
P2X7_MOUSE      ..SCTFHKAWDPOCSIFRLGDIFFQEAAGENFTEVAVQGGIMGIEIYWDCNLDWRFHHCRPR
P2X7_RAT        ..SCTFHKTWNPQCFIFRLGDIFFQEAAGENFTEVAVQGGIMGIEIYWDCNLDWRFHHCRPR
P2X2_HUMAN      LKRCITFHEASDLYCPIFKLGIFIVEKAGESFTELAKHGGVIGVLIINWDCDLDLPASECNP
P2X3_HUMAN      MKTCRFHPDKDPECPILRVGDVVKFAGQDFAKLARTGGVIGIKIGVCDLDKAWDQCIPK
P2X1_HUMAN      MKTCLFHKTLHPLCPVFLQGLVQVQESQNFSTLAEKGGVIGITDWHCDLDWRFHHCRPI
P2X4_HUMAN      LKSCIDAKTDPECPIFRLGKIVENAGHSFQDMAVEGGIMGIEIYWDCNLDWRFHHCRPI
P2X5_HUMAN      LKSCHEGPKNH.YCPIFRLGKIVENAGHSFQDMAVEGGIMGIEIYWDCNLDWRFHHCRPI
P2X6_HUMAN      FKHCRIEPOFSYCPVFRIGDLVAKAGGTFFDLALLGGSVGIRVHWDCCDLDTGDSGCWPH

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FIG. 2B

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P2X7_HUMAN      YSFRRLDDKTTNVSLEYPGYNFRYAKYYKE.NNVEKRTLIKVFGRFDILVFGTGGKFDII
P2X7_VAR_HUMAN  .....YAKYYKE.NNVEKRTLIKVFGRFDILVFGTGGKFDII
P2X7_MOUSE      YSFRRLDDKNMDESFPVPGYNFRYAKYYKE.NNVEKRTLIKAFGRFDILVFGTGGKFDII
P2X7_RAT        YSFRRLDDKYTNESLPVPGYNFRYAKYYKE.NGMEKRTLIKAFGRFDILVFGTGGKFDII
P2X2_HUMAN      YSFRRLD..PKHVPASSGYNFRFAKYYKI.NGTTTRTLKAYGIRIDVIVHGOAGKFSII
P2X3_HUMAN      YSFTRLDSVSEKSSVSPGYNFRFAKYYKMENGSEYRTLKAFGRFDVLYVGNAGKFNII
P2X1_HUMAN      YEFHGLYE...EKNLSPGENFRFAHHEVE.NGTNYRHLEKVFGRFDILVDGKAGKFDII
P2X4_HUMAN      YSFRRLDTRDVEHNVSPGYNFRFAKYYRDLAGNEQRTLIKAYGIRFDIVFGKAGKFDII
P2X5_HUMAN      YSESRLDNK.LSKSVSSGYNFRFAYYRDAAGVEFRTLMKAYGIRFDMVNGK.GAF...
P2X6_HUMAN      YSEQ.LQEK.....SYNFRTATHWWEQPGVEARTLLKLYGIRFDILVTGOAGKFGII

P2X7_HUMAN      QLVVYIGSTLSYFGLAAVFIDFLIDTY..SSNCCRSHIYPWCKCCQPCVVNEYMYRKKCE
P2X7_VAR_HUMAN  QLVVYIGSTLSYFGLATVFIDFLIDTY..SSNCCRSHIYPWCKCCQPCVVNEYMYRKKCE
P2X7_MOUSE      QLVVYIGSTLSYFGLATVCIDLIIINTY..SSAFCRSGVYPYCKCCEPCTVNEYMYRKKCE
P2X7_RAT        QLVVYIGSTLSYFGLATVCIDLIIINTY..ASTCCRSRVYPSCKCCEPCAVNEYMYRKKCE
P2X2_HUMAN      PTIINLATALTSVGVSFLCDWILLTFMNKNKVYSHKKEDKVCTPSHPSGSWPVTLARVL
P2X3_HUMAN      PTIISVAAFISVGVTVLCDIILLNFKGADQYKAKKEEV.....NETTLKIAALT
P2X1_HUMAN      PTMTTIGSGTIGIFGVATVLCDLLLHILPKRHYYKQKKEKYAEDMGPG.AA.ERDLAATS
P2X4_HUMAN      PTMINIGSLALLGMATVLCDLIVLYCMKKRLYYREKKYKYVEDYEQGLAS.ELDQ~~~
P2X5_HUMAN      .....FCDLVLLIYLTKKRETYRDKKYEVEVGLDEDSSQE.AEDEA...
P2X6_HUMAN      PTAVTLEGTGAAWLGVTFFCDLLLLLYVDREAHFYWRTKYEEAKAPKATANS.VWRELALA

P2X7_HUMAN      SIVEPKPTLKYSFVDESHIRMVNQQLL..GRSLQDVKGQEVPRFAMDFDLSRLPLALH
P2X7_VAR_HUMAN  SIVEPKPTLKYSFVDESHIRMVNQQLL..GRSLQDVKGQEVPRFAMDFDLSRLPLALH
P2X7_MOUSE      SIMEPKPTLKYSFVDEPHIRMVNQQLL..GKSLQVVKGOEVPREPQDFSDLSRLSLSLH
P2X7_RAT        PIVEPKPTLKYSFVDEPHIWMVQQLL..GKSLQDVKGQEVPRPQDFLELSRLSLSLH
P2X2_HUMAN      GOAPPEPGHRSSEQHPSPPSGQEQGGAECGPAFPPLRCPPTSAPEQMVDTPAPEPAQA
P2X3_HUMAN      NPVYVSDQTAEKQSTDSGAFSIGH~~~~~
P2X1_HUMAN      STLGLQENMRTS~~~~~
P2X4_HUMAN      ~~~~~
P2X5_HUMAN      SGLGLSEQLTSGPGILGMPEQQELQEPPEAKRGSSSQKNGSVCPOTLEPHRST~~~~~
P2X6_HUMAN      SQARLAECLEERSAPAPTATAAGSQQTQTPGWPCPSSDTHLPTHSGST~~~~~

P2X7_HUMAN      DTPPIPGQPEETQLLRKEATPRSRDSPVWCQCGSCLPSQLPESHRCLEELCCRKPGACI
P2X7_VAR_HUMAN  DTPPIPGQPEETQLLRKEATPRSRDSPVWCQCGSCLPSQLPESHRCLEELCCRKPGACI
P2X7_MOUSE      DSPLTPGQSEETQLLHEEVAPKSGDSPWCQCGNCLPSRLPEQRRALEELCCRKPGRCI
P2X7_RAT        HSPPIPGQPEEMQLLQIEAVPRSRDSPWCQCGNCLPSQLPENRRALEELCCRKPGQCI
P2X2_HUMAN      SITPTDEKGLAQL~~~~~
P2X3_HUMAN      ~~~~~
P2X1_HUMAN      ~~~~~
P2X4_HUMAN      ~~~~~
P2X5_HUMAN      ~~~~~
P2X6_HUMAN      ~~~~~

P2X7_HUMAN      TTSELFRLKLVLSRHVLQFLLLYQEPLLALDVDSTNSRLRHCA YRCYATWRFSGQDMADFA
P2X7_VAR_HUMAN  TTSELFRLKLVLSRHVLQFLLLYQEPLLALDVDSTNSRLRHCA YRCYATRRFSGQDMADFA
P2X7_MOUSE      TTSKLFHKLVLSDRTLQLLLLLYQDPLLVLGEEATNSRLRHRA YRCYATWRFSGQDMADFA
P2X7_RAT        TTSELFKIVLSREALQLLLLLYQEPLLALGEA INSKLRHCA YRSYATWRFVSGQDMADFA
P2X2_HUMAN      ~~~~~
P2X3_HUMAN      ~~~~~
P2X1_HUMAN      ~~~~~
P2X4_HUMAN      ~~~~~
P2X5_HUMAN      ~~~~~
P2X6_HUMAN      ~~~~~

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FIG. 2C

P2X7_HUMAN	ILPSCCRWRIRKEFPKSEGQYSGFKSPY~
P2X7_VAR_HUMAN	ILPSCCRWRIRKEFPKSEGQYSGFKSPY*
P2X7_MOUSE	ILPSCCRWRIRKEFPKTEGQYSGFKYPY~
P2X7_RAT	ILPSCCRWKIRKEFPKTQGQYSGFKYPY~
P2X2_HUMAN	~~~~~
P2X3_HUMAN	~~~~~
P2X1_HUMAN	~~~~~
P2X4_HUMAN	~~~~~
P2X5_HUMAN	~~~~~
P2X6_HUMAN	~~~~~

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FIG. 3

D = P2X\_receptor PF00864 ATP P2X receptor

Identical Match = 118 Similar = 194 Total # Of Gaps = 14

Identity: Alignment = 28% Query = 23% Target = 30%

Similarity: Alignment = 46% Query = 38% Target = 49%

QS = 11 QE = 315 TS = 1 TE = 395

Q: P2X7 VARIANT; T:P2X7 HMM Model

```

Q      11 FQYETNKVTRIQSMNYGTIKWFFHVIIFSVC-F-----ALVSDKLYQRKEP
      F Y+T K+  + +   G +       +I +Y+          +++ K YQ  +
T      1 FDYKTPKYVVVRNWKVGLMYRMVQLLILVYFVGWVASGAGTALSHRYVFLWEKGYQDRDT

Q      57 -VISSVHTKVKGIA--EVKEEIVENGVKKLVSFVDTADYTFPLQG-NSFFVMTNFLKTE
      ++SSV TKVKG+A  +V +       +++L   V D ADY +P QG N+FFVMTN++ T+
T      61 SPQSSVITKVKGVAMTNVTQ-----TSMLGNRVWDVADYVIPPOGENVFFVMTNMIVTP

Q     113 GQEQRLCPEYPTR-RTLCSSDRGCKKGWMDPQSKGIQTGRCVVYEGNQK-TCEVSAWCPI
      Q Q +CPE P   ++ C+SD +C  G  + ++ GI TGRCV++++  + TCE++AWCP+
T     115 NQTQGYCPEHPEVPDGNCSWSDSDCHAGEAGMHGHGIKTGRCVRFNHSRRTCEIWAACPV

Q     171 EAVEEAPRPALLNSAENFTVLIKNNIDFP-----
      E  +  P+P++L  AENFT +IKN+I FP
T     175 EDDDHVPMPPMLKEAENFTIFIKNSIWFPKFNFSKRNIENWNDTYMKHCHFHPKNHPYC

Q     200 -----GHNYTT-----Y-----
      G++ ++                      +
T     235 PIFRLGDIVEWAGQDFQDLAHKGGVIGIQINWDCDLDAWSHCWPHYSFHRLDNRKHEHN

Q     207 -----AKYYKEN-NVEKRTLIKVFGRFDILVFGTGGKFDDIQLVVYIGSTLSYFG
      AKYY++N  VE RTL+K++GIRFD++V+G  GKFDII  ++ IGS L  +G
T     295 VSPGYNFRFAKYYWDNNGVEYRTLKAYGIRFDVIVHGKAGKFDDIPTMINIGSGLAWMG

Q     257 LATVFIDFLIDTYSSNCCRSHIYPWCKCCQPCVVNEYYYRKKCESIVEPKPTLKYSFV
      +T+F D +                +Y  K          +YY +KK E   ++K+++  +
T     355 VGTFFCDWIL-----LYCMKK-----RHYYWHKKFEYVEDMKQGANSEWEA

```

FIG. 4

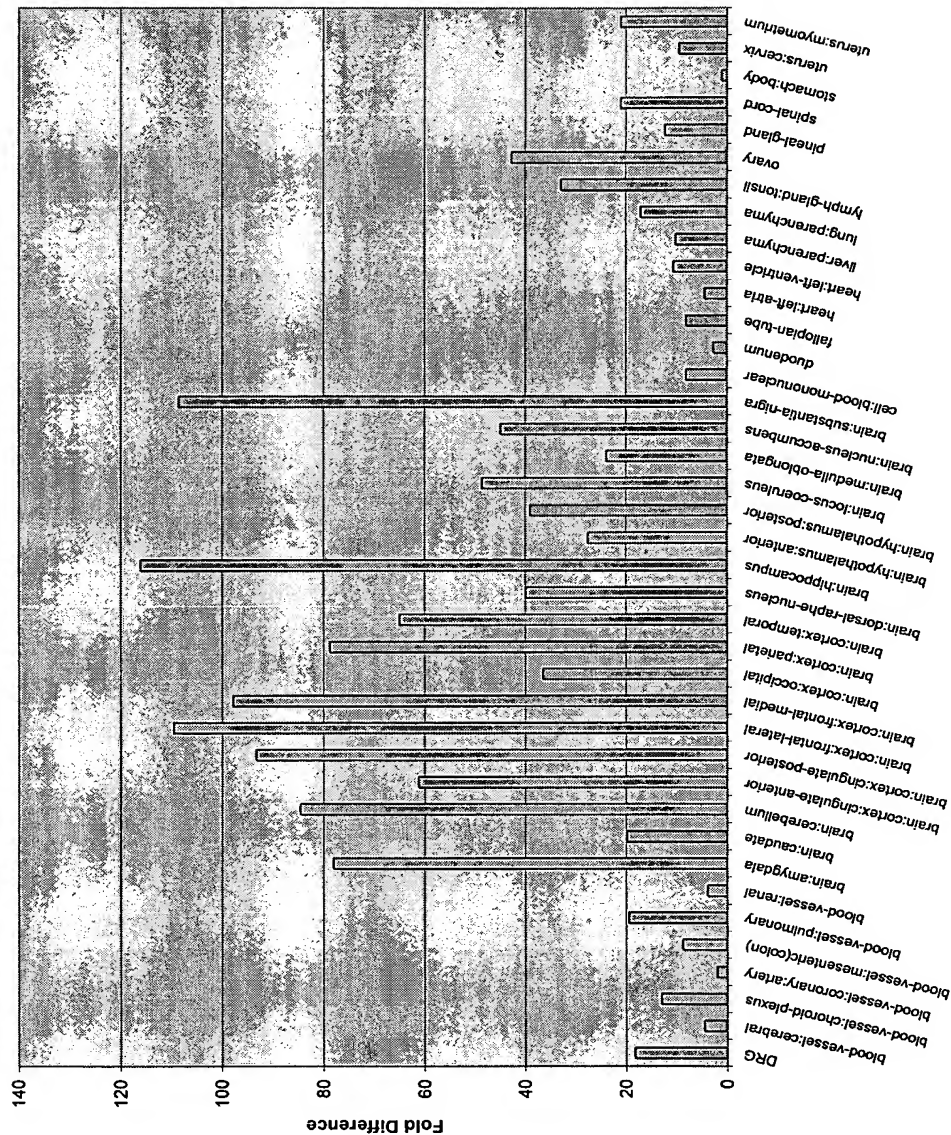




FIG. 5

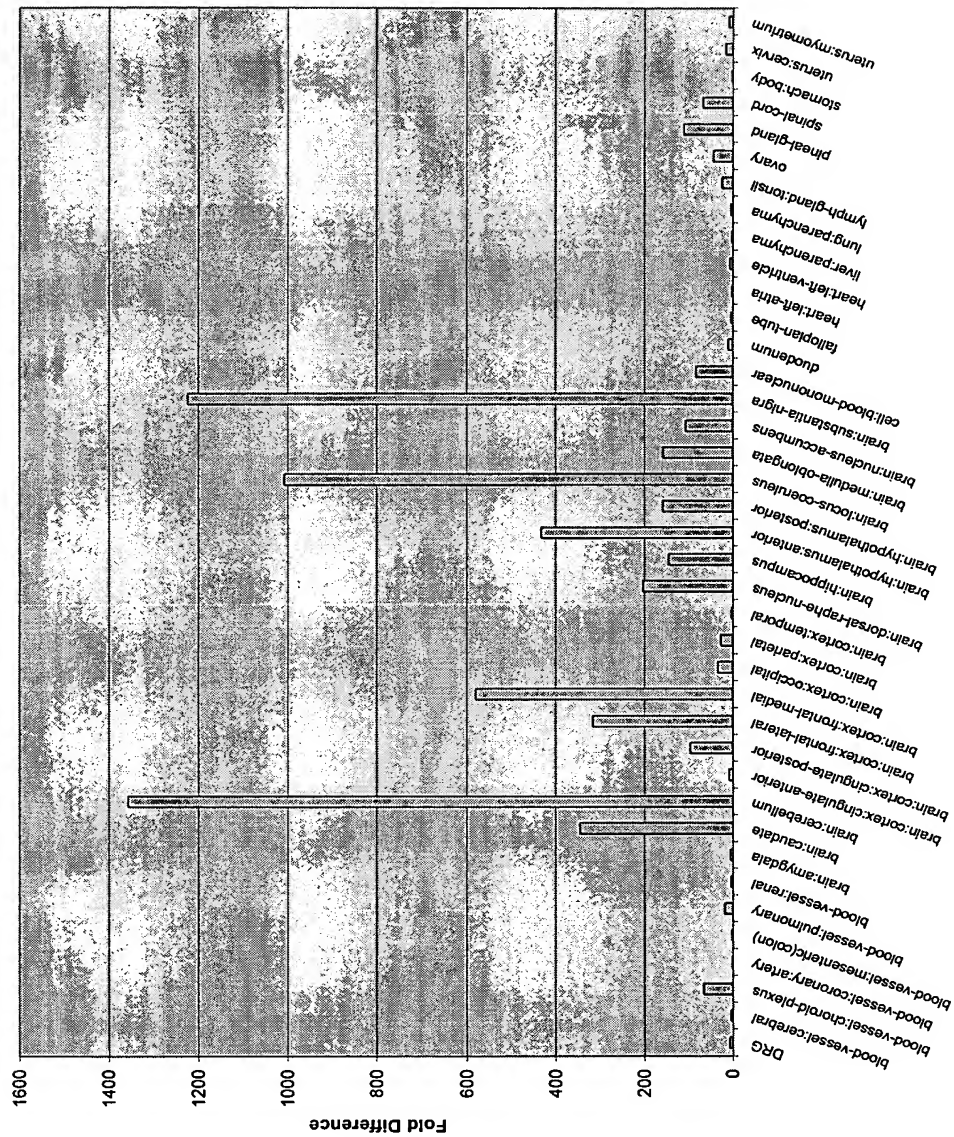


FIG. 6

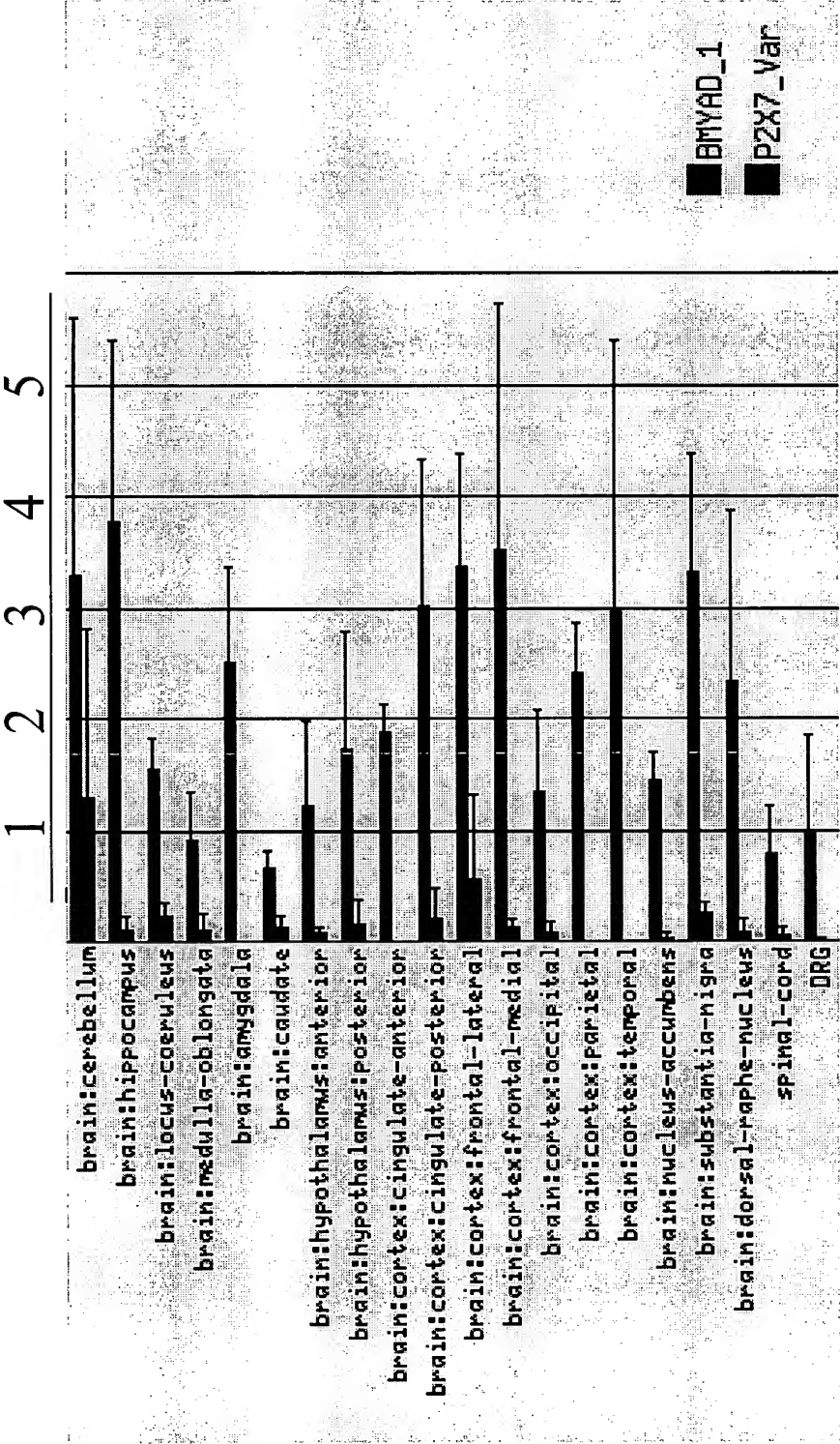
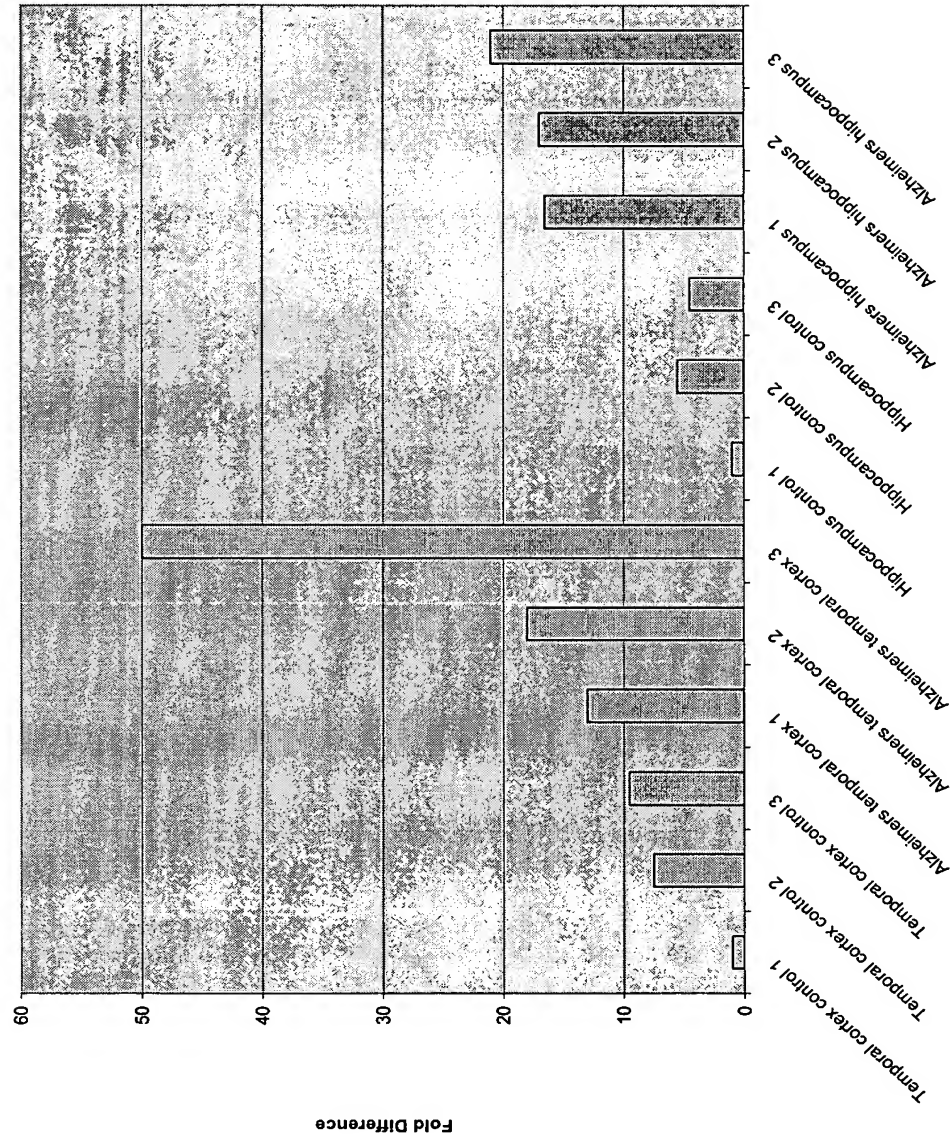


FIG. 7



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**FIG. 8**

Protein	Genbank/ SWISS-PROT Accession	Identities	Similarities
human P2X7 protein	Q99572	84.4%	84.5%
mouse P2X7 protein	Q9Z1M0	69.4%	73.3%
rat P2X7 protein	Q64663	67.9%	73.4%
human P2X2 protein	Q9UBL9	19.4%	29.5%
human P2X3 protein	P56373	19.6%	28.1%
human P2X1 protein	P51575	19.4%	30.5%
human P2X4 protein	Q99571	22.6%	32.2%
human P2X5 protein	Q93086	19.8%	27.8%
human P2X6 protein	O15547	20.6%	32.4%